



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Weiner, Howard
Miller, Ariel
Zheng, Zhengi
Al-Sabbagh, Ahmad

(ii) TITLE OF INVENTION: BYSTANDER SUPPRESSION OF AUTOIMMUNE DISEASES

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: U.S.A.
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/461,662
(B) FILING DATE: 05-JUN-1995
(C) CLASSIFICATION: 424

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/843,752
(B) FILING DATE: 28-FEB-1992

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 1010/16959-US5

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bos taurus

(F) TISSUE TYPE: PLP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly	Leu	Leu	Gly	Cys	Cys	Ala	Arg	Cys	Leu	Val	Gly	Ala	Pro	Phe	Ala	
1				5					10					15		
Ser	Leu	Val	Ala	Thr	Gly	Leu	Cys	Phe	Phe	Gly	Val	Ala	Leu	Phe	Cys	
			20					25					30			
Gly	Cys	Gly	His	Glu	Ala	Leu	Thr	Gly	Thr	Glu	Lys	Leu	Ile	Glu	Thr	
		35					40					45				
Tyr	Phe	Ser	Lys	Asn	Tyr	Gln	Asp	Tyr	Glu	Tyr	Leu	Ile	Asn	Val	Ile	
	50					55					60					
His	Ala	Phe	Gln	Tyr	Val	Ile	Tyr	Gly	Thr	Ala	Ser	Phe	Phe	Phe	Leu	
65					70					75					80	
Tyr	Gly	Ala	Leu	Leu	Leu	Ala	Tyr	Gly	Phe	Tyr	Thr	Thr	Gly	Ala	Val	
			85						90					95		
Arg	Gln	Ile	Phe	Gly	Asp	Tyr	Lys	Thr	Thr	Ile	Cys	Gly	Lys	Gly	Leu	
			100					105					110			
Ser	Ala	Thr	Val	Thr	Gly	Gly	Gln	Lys	Gly	Arg	Gly	Ser	Arg	Gly	Gln	
		115					120					125				
His	Gln	Ala	His	Ser	Leu	Glu	Arg	Val	Cys	His	Cys	Leu	Gly	Lys	Trp	
	130					135					140					
Leu	Gly	His	Pro	Asp	Lys	Phe	Val	Gly	Ile	Thr	Tyr	Ala	Leu	Thr	Val	
145					150					155					160	
Val	Trp	Leu	Leu	Val	Phe	Ala	Cys	Ser	Ala	Val	Pro	Val	Tyr	Ile	Tyr	
			165						170					175		
Phe	Asn	Thr	Trp	Thr	Thr	Cys	Gln	Ser	Ile	Ala	Ala	Pro	Ser	Lys	Thr	
			180					185					190			
Ser	Ala	Ser	Ile	Gly	Thr	Leu	Cys	Ala	Asp	Ala	Arg	Met	Tyr	Gly	Val	
		195					200					205				
Leu	Pro	Trp	Asn	Ala	Phe	Pro	Gly	Lys	Val	Cys	Gly	Ser	Asn	Leu	Leu	
	210					215					220					

Ser	Ile	Cys	Lys	Thr	Ala	Glu	Phe	Gln	Met	Thr	Phe	His	Leu	Phe	Ile
225					230					235					240
Ala	Ala	Phe	Val	Gly	Ala	Ala	Ala	Thr	Leu	Val	Ser	Leu	Val	Thr	Phe
				245					250					255	
Met	Ile	Ala	Ala	Thr	Tyr	Asn	Phe	Ala	Val	Leu	Lys	Leu	Met	Gly	Arg
			260					265					270		
Gly	Thr	Lys	Phe												
			275												

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: insulin
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly	Ile	Val	Glu	Gln	Cys	Cys	Thr	Ser	Ile	Cys	Ser	Leu	Tyr	Gln	Leu
1				5					10					15	
Glu	Asn	Tyr	Cys	Asn											
			20												

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(F) TISSUE TYPE: insulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(F) TISSUE TYPE: MBP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala
1 5 10 15

Thr Ala Ser Thr Met Asp Asn Ala Arg Asn Gly Phe Leu Pro Arg Asn
20 25 30

Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly Asp
35 40 45

Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser Met Met Pro Ala
50 55 60

Arg Thr Ala Met Tyr Gly Ser Leu Pro Gln Lys Ser Asn Gly Arg Thr
65 70 75 80

Gln Asp Glu Asn Pro Val Val Met Phe Phe Lys Met Ile Val Thr Pro
85 90 95

Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser
100 105 110

Arg Phe Ser Trp Gly Ala Glu Ser Gln Arg Arg Pro Gly Phe Gly Tyr
115 120 125

Gly	Gly	Arg	Ala	Ser	Asp	Tyr	Lys	Ser	Ala	Met	Lys	Gly	Phe	Lys	Gly
130						135					140				
Val	Asp	Ala	Gln	Gly	Thr	Leu	Ser	Lys	Ile	Phe	Lys	Leu	Gly	Gly	Arg
145					150					155					160
Asp	Ser	Arg	Ser	Gly	Ser	Pro	Met	Ala	Arg	Arg					
				165					170						

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bos taurus
- (F) TISSUE TYPE: MBP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala	Ala	Gln	Lys	Arg	Pro	Ser	Gln	Arg	Ser	Lys	Tyr	Leu	Ala	Ser	Ala
1				5					10					15	
Ser	Thr	Lys	Asp	Met	Ala	Arg	Met	Gly	Pro	Leu	Pro	Arg	Asn	Arg	Asp
			20					25					30		
Thr	Gly	Ile	Leu	Asp	Ser	Leu	Gly	Arg	Phe	Phe	Gly	Ser	Asp	Arg	Gly
		35					40					45			
Ala	Pro	Lys	Arg	Gly	Ser	Gly	Ser	Gly	Lys	Asp	Gly	Met	Met	Ala	Ala
	50					55					60				
Arg	Thr	Thr	Met	Tyr	Gly	Ser	Leu	Pro	Gln	Lys	Ala	Gln	His	Gly	Arg
65					70					75					80
Pro	Gln	Asp	Glu	Asn	Pro	Val	Val	Met	Phe	Phe	Lys	Asn	Ile	Val	Thr
				85					90					95	
Pro	Arg	Thr	Pro	Pro	Pro	Ser	Gln	Gly	Lys	Gly	Arg	Gly	Leu	Ser	Leu
			100					105					110		
Ser	Arg	Phe	Ser	Trp	Gly	Ala	Glu	Gly	Gln	Lys	Pro	Gly	Phe	Gly	Tyr
		115					120					125			
Gly	Gly	Arg	Ala	Ser	Asp	Tyr	Lys	Ser	Ala	Asn	Lys	Gly	Leu	Lys	Gly
	130					135					140				

Met Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg
145 150 155 160

Asp Ser Arg Ser Gly Ser Pro Met Ala Arg Arg
165 170

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Oryctolagus cuniculus*

(F) TISSUE TYPE: MBP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala	Ser	Gln	Lys	Arg	Pro	Ser	Gln	Arg	Asn	Gly	Ser	Lys	Tyr	Leu	Ala	1	5	10	15
Thr	Ala	Ser	Thr	Met	Asp	Met	Ala	Arg	Met	Gly	Phe	Arg	Asn	Arg	Asp	20	25	30	
Thr	Gly	Ile	Leu	Asp	Ser	Ile	Gly	Arg	Phe	Phe	Ser	Ser	Asp	Arg	Gly	35	40	45	
Ala	Pro	Lys	Arg	Gly	Ser	Gly	Lys	Asp	Met	Ala	Arg	Thr	Thr	Met	Tyr	50	55	60	
Gly	Ser	Leu	Pro	Gln	Lys	Ser	Asn	Gly	Arg	Pro	Gln	Asp	Glu	Asn	Pro	65	70	75	80
Val	Val	Met	Phe	Phe	Lys	Asn	Ile	Val	Thr	Arg	Pro	Thr	Pro	Pro	Pro	85	90	95	
Ser	Gln	Gly	Lys	Gly	Arg	Gly	Thr	Val	Leu	Ser	Arg	Phe	Ser	Trp	Gly	100	105	110	
Ala	Glu	Gly	Gln	Lys	Pro	Gly	Phe	Gly	Tyr	Gly	Gly	Arg	Ala	Ala	Asp	115	120	125	
Tyr	Lys	Ser	Ala	Asn	Lys	Gly	Leu	Lys	Gly	Ala	Asp	Ala	Gln	Gly	Thr	130	135	140	
Leu	Leu	Ser	Arg	Leu	Phe	Lys	Gly	Gly	Arg	Asp	Ser	Arg	Ser	Gly	Ser	145	150	155	160

Gly Ser Pro Met Ala Arg Arg
165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 166 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cavia porcellus*

(F) TISSUE TYPE: MBP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Ser Gln Lys Arg Pro Ser Gln Arg Met Gly Ser Lys Tyr Leu Ala
1 5 10 15

Thr Ala Ser Thr Met Asp Met Ala Arg Met Gly Phe Leu Pro Arg Asn
20 25 30

Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Ser Asp
35 40 45

Arg Ala Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser Met Ala Ala Arg
50 55 60

Thr Thr Met Tyr Gly Ser Leu Pro Gln Lys Ser Gln Arg Ser Gln Asp
65 70 75 80

Glu Asn Pro Val Val Asn Phe Phe Xaa Asn Ile Val Thr Pro Arg Thr
85 90 95

Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser Arg Phe
100 105 110

Ser Trp Gly Ala Glu Ser Gln Lys Pro Gly Phe Gly Tyr Gly Gly Arg
115 120 125

Ala Asp Tyr Lys Ser Lys Gly Phe Lys Gly Ala Met Asp Ala Gln Gly
130 135 140

Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg Asp Ser Arg Ser Gly
145 150 155 160

Ser Pro Met Ala Arg Arg
165

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus sordidus
- (F) TISSUE TYPE: MBP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Ser	Gln	Lys	Arg	Pro	Ser	Gln	Arg	Met	Gly	Ser	Lys	Tyr	Leu	Ala	
1				5					10					15		
Thr	Ala	Ser	Thr	Met	Asp	Asn	Ala	Arg	Met	Gly	Phe	Leu	Pro	Arg	Met	
			20					25					30			
Arg	Asp	Thr	Gly	Ile	Leu	Asp	Ser	Ile	Gly	Arg	Phe	Phe	Ser	Gly	Asp	
		35					40					45				
Arg	Gly	Ala	Pro	Lys	Arg	Gly	Ser	Gly	Lys	Asp	Ser	Met	Thr	Arg	Thr	
	50					55					60					
Thr	Met	Tyr	Gly	Ser	Leu	Pro	Gln	Lys	Ser	Gln	Arg	Thr	Gln	Asp	Glu	
65					70					75					80	
Asn	Pro	Val	Val	Met	Phe	Phe	Lys	Met	Ile	Val	Thr	Pro	Arg	Thr	Pro	
				85					90					95		
Pro	Pro	Ser	Gln	Gly	Lys	Gly	Arg	Gly	Leu	Ser	Leu	Ser	Arg	Phe	Ser	
			100					105					110			
Trp	Gly	Gly	Arg	Asp	Ser	Arg	Ser	Gly	Ser	Pro	Met	Ala	Arg	Arg		
		115					120					125				

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Gallus domesticus

(F) TISSUE TYPE: MBP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala	Ser	Gln	Lys	Arg	Ser	Ser	Phe	Arg	Asn	Gly	Ser	Lys	Met	Ala	Ser	
1				5					10					15		
Ala	Thr	Ser	Thr	Asp	Met	Ala	Arg	Met	Gly	Ser	Pro	Arg	Met	Arg	Asp	
			20					25					30			
Ser	Gly	Leu	Leu	Asp	Ser	Leu	Gly	Arg	Phe	Phe	Gly	Ser	Asp	Arg	Val	
		35					40					45				
Pro	Lys	Arg	Gly	Phe	Gly	Lys	Asp	Ala	Ala	Arg	Ala	Ser	Met	Val	Gly	
	50					55					60					
Ser	Ile	Pro	Gln	Arg	Ser	Gln	Met	Arg	Pro	Met	Asp	Gly	Met	Pro	Val	
65					70					75					80	
Val	Met	Phe	Phe	Lys	Asn	Ile	Val	Ser	Pro	Arg	Thr	Pro	Pro	Pro	Met	
				85					90					95		
Gln	Ala	Lys	Gly	Arg	Gly	Leu	Ser	Leu	Thr	Arg	Phe	Ser	Trp	Gly	Gly	
			100					105					110			
Glu	Gly	Met	Lys	Pro	Gly	Ser	Gly	Tyr	Gly	Gly	Lys	Phe	Tyr	Glu	Asn	
		115					120					125				
Lys	Ser	Ala	Met	Lys	Gly	His	Lys	Gly	Tyr	Ser	Met	Gln	Gly	Glu	Gly	
	130					135					140					
Thr	Leu	Ser	Lys	Ile	Phe	Lys	Leu	Gly	Gly	Arg	Pro	Ser	Gly	Ser	Gly	
145					150					155					160	
Ser	Arg	Ser	Gly	Ser	Pro	Val	Ala	Arg	Arg							
				165					170							

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1017 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(F) TISSUE TYPE: collagen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly	Pro	Met	Gly	Pro	Met	Gly	Pro	Arg	Gly	Pro	Pro	Gly	Pro	Ala	Gly	
1				5					10					15		
Ala	Pro	Gly	Pro	Gln	Gly	Phe	Gln	Gly	Asn	Pro	Gly	Glu	Pro	Gly	Glu	
			20					25					30			
Pro	Gly	Val	Ser	Gly	Pro	Met	Gly	Pro	Arg	Gly	Pro	Pro	Gly	Pro	Pro	
		35					40					45				
Gly	Lys	Pro	Gly	Asp	Asp	Gly	Glu	Ala	Gly	Lys	Pro	Gly	Lys	Ala	Gly	
	50					55					60					
Glu	Arg	Gly	Pro	Pro	Gly	Pro	Gln	Gly	Ala	Arg	Gly	Phe	Pro	Gly	Thr	
65					70					75					80	
Pro	Gly	Leu	Pro	Gly	Val	Lys	Gly	His	Arg	Gly	Tyr	Pro	Gly	Leu	Asp	
				85					90					95		
Gly	Ala	Lys	Gly	Glu	Ala	Gly	Ala	Pro	Gly	Val	Lys	Gly	Glu	Ser	Gly	
			100					105					110			
Ser	Pro	Gly	Glu	Asn	Gly	Ser	Pro	Gly	Pro	Met	Gly	Pro	Arg	Gly	Leu	
		115					120					125				
Pro	Gly	Glu	Arg	Gly	Arg	Thr	Gly	Pro	Ala	Gly	Ala	Ala	Gly	Ala	Arg	
	130					135					140					
Gly	Asn	Lys	Gly	Gln	Pro	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Pro	Val	Gly	
145					150					155					160	
Pro	Ala	Gly	Gly	Pro	Gly	Phe	Pro	Gly	Ala	Pro	Gly	Ala	Lys	Gly	Glu	
				165					170					175		
Ala	Gly	Pro	Thr	Gly	Ala	Arg	Gly	Pro	Glu	Gly	Ala	Gln	Gly	Pro	Arg	
			180					185					190			
Gly	Glu	Pro	Gly	Thr	Pro	Gly	Ser	Pro	Gly	Pro	Ala	Gly	Ala	Ser	Gly	
		195					200					205				
Asn	Pro	Gly	Thr	Lys	Gly	Ile	Pro	Gly	Ala	Lys	Gly	Ser	Ala	Gly	Ala	
	210					215					220					
Pro	Gly	Ile	Ala	Gly	Ala	Pro	Gly	Phe	Pro	Gly	Pro	Arg	Gly	Pro	Pro	
225					230					235					240	
Lys	Pro	Gln	Gly	Ala	Thr	Gly	Pro	Leu	Gly	Pro	Lys	Gly	Gln	Thr	Gly	
				245					250					255		

Lys Pro Gly Ile Ala Gly Phe Lys Gly Glu Gln Gly Pro Lys Gly Glu
 260 265 270
 Pro Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Pro Ala Gly Glu Glu
 275 280 285
 Gly Lys Arg Gly Ala Arg Gly Gln Pro Gly Gly Val Gly Pro Ile Gly
 290 295 300
 Pro Pro Gly Gln Arg Gly Ala Pro Gly Asn Arg Gly Phe Pro Gly Gln
 305 310 315 320
 Asp Gly Leu Ala Gly Pro Lys Gly Ala Pro Gly Glu Arg Gly Pro Ser
 325 330 335
 Gly Leu Ala Gly Pro Lys Gly Ala Asn Gly Asp Pro Gly Arg Pro Gly
 340 345 350
 Glu Pro Gly Leu Pro Gly Ala Arg Gly Leu Thr Gly Arg Pro Gly Asp
 355 360 365
 Ala Gly Pro Gln Gly Lys Val Gly Pro Ser Gly Ala Pro Gly Glu Asp
 370 375 380
 Gly Arg Pro Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Gln Pro Gly
 385 390 395 400
 Val Met Gly Phe Pro Gly Pro Lys Gly Ala Asn Gly Glu Pro Gly Lys
 405 410 415
 Ala Gly Glu Lys Gly Leu Pro Gly Ala Pro Gly Leu Arg Gly Leu Pro
 420 425 430
 Gly Lys Asp Gly Glu Thr Gly Ala Glu Gly Pro Pro Gly Pro Ala Gly
 435 440 445
 Pro Ala Gly Glu Arg Gly Glu Gln Gly Ala Pro Gly Pro Ser Gly Phe
 450 455 460
 Gln Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Glu Ala Gly Lys Pro
 465 470 475 480
 Gly Asp Gln Gly Val Pro Gly Glu Ala Gly Ala Pro Gly Leu Val Gly
 485 490 495
 Pro Arg Gly Glu Arg Gly Phe Pro Gly Glu Arg Gly Ser Pro Gly Ala
 500 505 510
 Gln Gly Leu Gln Gly Pro Arg Gly Leu Pro Gly Thr Pro Gly Thr Asp
 515 520 525
 Gly Pro Lys Gly Ala Ser Gly Pro Ala Gly Pro Pro Gly Ala Gln Gly
 530 535 540

Pro 545	Pro	Gly	Leu	Gln	Gly 550	Met	Pro	Gly	Glu	Arg 555	Gly	Ala	Ala	Gly	Ile 560
Ala	Gly	Pro	Lys	Gly 565	Asp	Arg	Gly	Asp	Val 570	Gly	Glu	Lys	Gly	Pro	Glu 575
Gly	Ala	Pro	Gly 580	Lys	Asp	Gly	Ala	Arg 585	Gly	Leu	Thr	Gly	Pro	Ile	Gly 590
Pro	Pro	Gly 595	Pro	Ala	Gly	Ala	Asn 600	Gly	Glu	Lys	Gly	Glu	Val	Gly	Pro
Pro	Gly 610	Pro	Ala	Gly	Ser	Ala 615	Gly	Ala	Arg	Gly	Ala 620	Pro	Gly	Glu	Arg
Gly 625	Glu	Thr	Gly	Pro	Pro 630	Gly	Pro	Ala	Gly	Phe 635	Ala	Gly	Pro	Pro	Gly 640
Ala	Asp	Gly	Gln	Pro 645	Gly	Ala	Lys	Gly	Glu 650	Gln	Gly	Glu	Ala	Gly	Gln 655
Lys	Gly	Asp	Ala 660	Gly	Ala	Pro	Gly	Pro	Gln 665	Gly	Pro	Ser	Gly	Ala	Pro 670
Gly	Pro	Gln 675	Gly	Pro	Thr	Gly	Val 680	Thr	Gly	Pro	Lys	Gly	Ala	Arg	Gly 685
Ala 690	Gln	Gly	Pro	Pro	Gly	Ala 695	Thr	Gly	Phe	Pro	Gly	Ala	Ala	Gly	Arg 700
Val 705	Gly	Pro	Pro	Gly	Ser 710	Asn	Gly	Asn	Pro	Gly 715	Pro	Pro	Gly	Pro	Pro 720
Gly	Pro	Ser	Gly	Lys 725	Asp	Gly	Pro	Lys	Gly 730	Ala	Arg	Gly	Asp	Ser	Gly 735
Pro	Pro	Gly	Arg 740	Ala	Gly	Glu	Pro	Gly 745	Leu	Gln	Gly	Pro	Ala	Gly	Pro 750
Pro	Gly	Glu 755	Lys	Gly	Glu	Pro	Gly 760	Asp	Asp	Gly	Pro	Ser	Gly	Ala	Glu 765
Gly 770	Pro	Pro	Gly	Pro	Gln	Gly 775	Leu	Ala	Gly	Gln	Arg 780	Gly	Ile	Val	Gly
Leu 785	Pro	Gly	Gln	Arg	Gly 790	Glu	Arg	Gly	Phe	Pro 795	Gly	Leu	Pro	Gly	Pro 800
Ser	Gly	Glu	Pro	Gly 805	Gln	Gln	Gly	Ala	Pro 810	Gly	Ala	Ser	Gly	Asp	Glu 815
Gly	Pro	Pro	Gly 820	Pro	Val	Gly	Pro	Pro 825	Gly	Leu	Thr	Gly	Pro	Ala	Gly 830

Glu	Pro	Gly	Arg	Glu	Gly	Ser	Pro	Gly	Ala	Asp	Gly	Pro	Pro	Gly	Arg	835	840	845
Asp	Gly	Ala	Ala	Gly	Val	Lys	Gly	Asp	Arg	Gly	Glu	Thr	Gly	Ala	Val	850	855	860
Gly	Ala	Pro	Gly	Ala	Pro	Gly	Pro	Pro	Gly	Ser	Pro	Gly	Pro	Ala	Gly	865	870	875
Pro	Thr	Gly	Lys	Gln	Gly	Asp	Arg	Gly	Glu	Ala	Gly	Ala	Gln	Gly	Pro	885	890	895
Met	Gly	Pro	Ser	Gly	Pro	Ala	Gly	Ala	Arg	Gly	Ile	Gln	Gly	Pro	Gln	900	905	910
Gly	Pro	Arg	Gly	Asp	Lys	Gly	Glu	Ala	Gly	Glu	Pro	Gly	Glu	Arg	Gly	915	920	925
Leu	Lys	Gly	His	Arg	Gly	Phe	Thr	Gly	Leu	Gln	Gly	Leu	Pro	Gly	Pro	930	935	940
Pro	Gly	Pro	Ser	Gly	Asp	Gln	Gly	Ala	Ser	Gly	Pro	Ala	Gly	Pro	Ser	945	950	955
Gly	Pro	Arg	Gly	Pro	Pro	Gly	Pro	Val	Gly	Pro	Ser	Gly	Lys	Asp	Gly	965	970	975
Ala	Asn	Gly	Ile	Pro	Gly	Pro	Ile	Gly	Pro	Pro	Gly	Pro	Arg	Gly	Arg	980	985	990
Ser	Gly	Glu	Thr	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Asn	Pro	Gly	Pro	Pro	995	1000	1005
Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Gly								1010	1015	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bos taurus
- (F) TISSUE TYPE: collagen (II)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly	Val	Met	Gly	Pro	Met	Gly	Pro	Arg	Gly	Pro	Pro	Gly	Pro	Ala	Gly	
1				5					10					15		
Ala	Pro	Gly	Pro	Gln	Gly	Phe	Gln	Gly	Asn	Pro	Gly	Glu	Pro	Gly	Glu	
			20					25					30			
Pro	Gly	Val	Ser	Gly	Pro	Met	Gly	Pro	Arg	Gly	Pro	Pro	Gly	Pro	Pro	
		35					40					45				
Gly	Lys	Pro	Gly	Asp	Asp	Gly	Glu	Ala	Gly	Lys	Pro	Gly	Lys	Ser	Gly	
	50					55					60					
Glu	Arg	Gly	Pro	Pro	Gly	Pro	Gln	Gly	Ala	Arg	Gly	Phe	Pro	Gly	Thr	
65					70					75					80	
Pro	Gly	Leu	Pro	Gly	Val	Lys	Gly	His	Arg	Gly	Tyr	Pro	Gly	Leu	Asp	
				85					90					95		
Gly	Ala	Lys	Gly	Glu	Gln	Gly	Ala	Pro	Gly	Val	Lys	Gly	Glu	Ser	Gly	
			100					105					110			
Ser	Pro	Gly	Glu	Asn	Gly	Ser	Pro	Gly	Pro	Met	Gly	Pro	Arg	Gly	Leu	
		115					120					125				
Pro	Gly	Glu	Arg	Gly	Arg	Thr	Gly	Pro	Ala	Gly	Ala	Ala	Gly	Ala	Arg	
	130					135					140					
Gly	Asn	Asp	Gly	Gln	Pro	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Pro	Val	Gly	
145					150					155					160	
Pro	Ala	Gly	Gly	Pro	Gly	Phe	Pro	Gly	Ala	Pro	Gly	Ala	Lys	Gly	Glu	
				165					170					175		
Ala	Gly	Pro	Thr	Gly	Ala	Arg	Gly	Pro	Glu	Gly	Ala	Gln	Gly	Pro	Arg	
			180					185					190			
Gly	Glu	Pro	Gly	Thr	Pro	Gly	Ala	Pro	Gly	Pro	Ala	Gly	Ala	Ala	Gly	
		195					200					205				
Asn	Pro	Gly	Ala	Asp	Gly	Ile	Pro	Gly	Ala	Lys	Gly	Ser	Ala	Gly	Ala	
	210					215					220					
Pro	Gly	Ile	Ala	Gly	Ala	Pro	Gly	Phe	Pro	Gly	Ala	Arg	Gly	Pro	Pro	
225					230					235					240	
Gly	Pro	Thr	Gly	Ala	Ser	Gly	Pro	Leu	Gly	Pro	Lys	Gly	Gln	Thr	Gly	
				245					250					255		
Lys	Pro	Gly	Ile	Ala	Gly	Phe	Lys	Gly	Glu	Gln	Gly	Pro	Lys	Gly	Glu	
			260					265					270			
Pro	Gly	Pro	Ala	Gly	Val	Gln	Gly	Ala	Pro	Gly	Pro	Ala	Gly	Glu	Glu	

275					280					285					
Gly	Lys	Arg	Gly	Ala	Arg	Gly	Glu	Pro	Gly	Gly	Ala	Gly	Pro	Ala	Gly
290						295					300				
Pro	Pro	Gly	Glu	Arg	Gly	Ala	Pro	Gly	Ser	Arg	Gly	Phe	Pro	Gly	Gln
305					310					315					320
Asp	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Pro	Gly	Glu	Arg	Gly	Ser	Pro
				325					330					335	
Gly	Ala	Val	Gly	Pro	Lys	Gly	Ser	Pro	Gly	Glu	Ala	Gly	Arg	Pro	Gly
			340					345					350		
Glu	Ala	Gly	Leu	Pro	Gly	Ala	Lys	Gly	Leu	Thr	Gly	Arg	Pro	Gly	Asp
		355					360					365			
Ala	Gly	Pro	Gln	Gly	Lys	Val	Gly	Pro	Ser	Gly	Ala	Pro	Gly	Glu	Asp
	370					375					380				
Gly	Arg	Pro	Gly	Pro	Pro	Gly	Pro	Gln	Gly	Ala	Arg	Gly	Gln	Pro	Gly
385					390					395					400
Val	Met	Gly	Phe	Pro	Gly	Pro	Lys	Gly	Ala	Asn	Gly	Glu	Pro	Gly	Lys
				405					410					415	
Ala	Gly	Glu	Lys	Gly	Leu	Pro	Gly	Ala	Pro	Gly	Thr	Asp	Gly	Pro	Lys
			420					425					430		
Gly	Ala	Ala	Gly	Pro	Ala	Gly	Ile	Ala	Gly	Pro	Lys	Gly	Asp	Arg	Gly
		435					440					445			
Asp	Val	Gly	Glu	Lys	Gly	Pro	Glu	Gly	Ala	Pro	Gly	Asp	Val	Gly	Glu
	450					455					460				
Lys	Gly	Glu	Val	Gly	Pro	Pro	Gly	Gln	Pro	Gly	Ala	Lys	Gly	Gly	Gln
465					470					475					480
Gly	Glu	Ala	Gly	Gln	Lys	Gly	Asp	Ala	Gly	Ala	Pro				
				485					490						

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bos taurus

(F) TISSUE TYPE: collagen (I)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Pro	Met	Gly	Pro	Ser	Gly	Pro	Arg	Gly	Leu	Pro	Gly	Pro	Pro	Gly	
1				5					10					15		
Ala	Pro	Gly	Pro	Gln	Gly	Phe	Gln	Gly	Pro	Pro	Gly	Glu	Pro	Gly	Glu	
			20					25					30			
Pro	Gly	Ala	Ser	Gly	Pro	Met	Gly	Pro	Arg	Gly	Pro	Pro	Gly	Pro	Pro	
		35					40					45				
Gly	Lys	Asn	Gly	Asp	Asp	Gly	Glu	Ala	Gly	Lys	Pro	Gly	Arg	Pro	Gly	
	50					55					60					
Glu	Arg	Gly	Pro	Pro	Gly	Pro	Gln	Gly	Ala	Arg	Gly	Leu	Pro	Gly	Thr	
65					70					75					80	
Ala	Gly	Leu	Pro	Gly	Met	Lys	Gly	His	Arg	Gly	Phe	Ser	Gly	Leu	Asp	
				85					90					95		
Gly	Ala	Lys	Gly	Asp	Ala	Gly	Pro	Ala	Gly	Pro	Lys	Gly	Glu	Pro	Gly	
			100					105					110			
Ser	Pro	His	Glu	Asn	Gly	Ala	Pro	Gly	Gln	Met	Gly	Pro	Arg	Gly	Leu	
		115					120					125				
Pro	Gly	Glu	Arg	Gly	Arg	Pro	Gly	Pro	Pro	Gly	Ser	Ala	Gly	Ala	Arg	
	130					135					140					
Gly	Asp	Asp	Gly	Ala	Val	Gly	Ala	Ala	Gly	Pro	Pro	Gly	Pro	Thr	Gly	
145					150					155					160	
Pro	Ala	Gly	Pro	Pro	Gly	Phe	Pro	Gly	Ala	Val	Gly	Ala	Lys	Gly	Glu	
				165					170					175		
Gly	Gly	Pro	Thr	Gly	Pro	Arg	Gly	Ser	Glu	Gly	Pro	Gln	Gly	Val	Arg	
			180					185					190			
Gly	Gln	Pro	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Ala	Ala	Gly	Pro	Ala	Gly	
		195					200					205				
Asn	Pro	Gly	Ala	Asp	Gly	Glu	Pro	Gly	Ala	Lys	Gly	Ala	Asn	Gly	Ala	
	210					215					220					
Pro	Gly	Ile	Ala	Gly	Ala	Pro	Gly	Phe	Pro	Gly	Ala	Arg	Gly	Pro	Ser	
225					230					235					240	
Gly	Pro	Gln	Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Asn	Ser	Gly	
				245					250					255		

Lys Pro Gly Ala Pro Gly Asn Lys Gly Asp Thr Gly Ala Lys Gly Glu
 260 265 270
 Pro Gly Pro Thr Gly Ile Gln Gly Pro Pro Gly Pro Ala Gly Glu Glu
 275 280 285
 Gly Lys Arg Gly Ala Arg Gly Glu Pro Gly Pro Thr Gly Leu Pro Gly
 290 295 300
 Pro Pro Gly Glu Arg Gly Gly Pro Gly Ser Arg Gly Phe Pro Gly Ala
 305 310 315 320
 Asp Gly Val Ala Gly Pro Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro
 325 330 335
 Gly Pro Ala Gly Pro Lys Gly Ser Pro Gly Glu Ala Gly Arg Pro Gly
 340 345 350
 Glu Ala Gly Leu Pro Gly Ala Lys Gly Leu Thr Gly Ser Pro Gly Ser
 355 360 365
 Pro Gly Pro Asp Gly Lys Thr Gly Pro Pro Gly Pro Ala Gly Gln Asn
 370 375 380
 Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Ala Arg Gly Gln Ala Gly
 385 390 395 400
 Val Met Gly Phe Pro Gly Pro Lys Gly Ala Ala Gly Glu Pro Gly Lys
 405 410 415
 Ala Gly Glu Arg Gly Val Pro Gly Pro Pro Gly Asn Asp Gly Ala Lys
 420 425 430
 Gly Asp Ala Gly Ala Pro Gly Leu Pro Gly Pro Lys Gly Asp Arg Gly
 435 440 445
 Asp Ala Gly Pro Lys Gly Ala Asp Gly Ala Pro Gly Ala Pro Gly Lys
 450 455 460
 Asp Gly Glu Ala Gly Pro Ser Gly Gln Pro Gly Ala Lys Gly Glu Pro
 465 470 475 480
 Gly Asp Ala Gly Ala Lys Gly Asp Ala Gly Ala Pro
 485 490

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bos tarus

(F) TISSUE TYPE: plp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys	Leu	Gly	Lys	Trp	Leu	Gly	His	Pro	Asp	Lys	Phe	Val	Gly	Ile	Thr
1				5					10					15	

Tyr	Ala	Leu	Thr	Val
			20	